



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/657,749C  
Source: \_\_\_\_\_  
Date Processed by STIC: 8/18/2003

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Revised 04/24/2003



1600

## RAW SEQUENCE LISTING

DATE: 08/18/2003

PATENT APPLICATION: US/08/657,749C

TIME: 13:10:45

Input Set : A:\1651802.app

Output Set: N:\CRF4\08182003\H657749C.raw

3 <110> APPLICANT: METZ, JAMES G.  
 4 LARDIZABAL, KATHRYN D.  
 5 LASSNER, MICHAEL  
 7 <120> TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING A PLANT CYTOPLASMIC  
 8 PROTEIN INVOLVED IN FATTY ACYL-COA METABOLISM  
 10 <130> FILE REFERENCE: 16518.025  
 12 <140> CURRENT APPLICATION NUMBER: 08/657,749C  
 13 <141> CURRENT FILING DATE: 1996-05-30  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US94/13686  
 16 <151> PRIOR FILING DATE: 1994-11-30  
 18 <150> PRIOR APPLICATION NUMBER: 08/265,047  
 19 <151> PRIOR FILING DATE: 1994-06-23  
 21 <150> PRIOR APPLICATION NUMBER: 08/160,602  
 22 <151> PRIOR FILING DATE: 1993-11-30  
 24 <150> PRIOR APPLICATION NUMBER: 08/066,299  
 25 <151> PRIOR FILING DATE: 1993-05-20  
 27 <150> PRIOR APPLICATION NUMBER: PCT/US92/09863  
 28 <151> PRIOR FILING DATE: 1992-11-13  
 30 <150> PRIOR APPLICATION NUMBER: 07/933,411  
 31 <151> PRIOR FILING DATE: 1992-08-21  
 33 <150> PRIOR APPLICATION NUMBER: 07/796,256  
 34 <151> PRIOR FILING DATE: 1991-11-20  
 36 <160> NUMBER OF SEQ ID NOS: 53  
 38 <170> SOFTWARE: PatentIn Ver. 2.1  
 40 <210> SEQ ID NO: 1  
 41 <211> LENGTH: 1786  
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 49 <220> FEATURE:  
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 52 <223> OTHER INFORMATION: a, c, t, or g  
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 56 <222> LOCATION: (1608)..(1609)  
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 62 gtagcaaaact taaaagaaa atg gag gaa atg gga agc att tta gag ttt ctt 112  
 63 Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu

Does Not Comply  
Corrected Discrete Needed

pr 5-8

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TIME: 13:10:45

Input Set : A:\1651802.app

Output Set: N:\CRF4\08182003\H657749C.raw

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67	Asp	Asn	Lys	Ala	Ile	Leu	Val	Thr	Gly	Ala	Thr	Gly	Ser	Leu	Ala	Lys	
68				15				20				25					
70	att	ttt	gtg	gag	aag	gta	ctg	agg	agt	caa	ccg	aat	gtg	aag	aaa	ctc	208
71	Ile	Phe	Val	Glu	Lys	Val	Leu	Arg	Ser	Gln	Pro	Asn	Val	Lys	Lys	Leu	
72			30					35				40					
74	tat	ctt	ctt	ttg	aga	gca	acc	gat	gac	gag	aca	gct	gct	cta	cgc	ttg	256
75	Tyr	Leu	Leu	Leu	Arg	Ala	Thr	Asp	Asp	Glu	Thr	Ala	Ala	Leu	Arg	Leu	
76		45						50				55					
78	caa	aat	gag	gtt	ttt	gga	aaa	gag	ttg	ttc	aaa	gtt	ctg	aaa	caa	aat	304
79	Gln	Asn	Glu	Val	Phe	Gly	Lys	Glu	Leu	Phe	Lys	Val	Leu	Lys	Gln	Asn	
80	60					65				70					75		
82	tta	ggt	gca	aat	ttc	tat	tcc	ttt	gta	tca	gaa	aaa	gtg	act	gta	gta	352
83	Leu	Gly	Ala	Asn	Phe	Tyr	Ser	Phe	Val	Ser	Glu	Lys	Val	Thr	Val	Val	
84					80					85				90			
86	ccc	ggt	gat	att	act	ggt	gaa	gac	ttg	tgt	ctc	aaa	gac	gtc	aat	ttg	400
87	Pro	Gly	Asp	Ile	Thr	Gly	Glu	Asp	Leu	Cys	Leu	Lys	Asp	Val	Asn	Leu	
88				95					100				105				
90	aag	gaa	gaa	atg	tgg	agg	gaa	atc	gat	gtt	gtt	gtc	aat	cta	gct	gct	448
91	Lys	Glu	Glu	Met	Trp	Arg	Glu	Ile	Asp	Val	Val	Val	Asn	Leu	Ala	Ala	
92			110					115				120					
94	aca	atc	aac	ttc	att	gaa	agg	tac	gac	gtg	tct	ctg	ctt	atc	aac	aca	496
95	Thr	Ile	Asn	Phe	Ile	Glu	Arg	Tyr	Asp	Val	Ser	Leu	Leu	Ile	Asn	Thr	
96		125				130				135							
98	tat	gga	gcc	aag	tat	gtt	ttg	gac	ttc	gcg	aag	aag	tgc	aac	aaa	tta	544
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100	140					145				150				155			
102	aag	ata	ttt	gtt	cat	gta	tct	act	gct	tat	gta	tct	gga	gag	aaa	aat	592
103	Lys	Ile	Phe	Val	His	Val	Ser	Thr	Ala	Tyr	Val	Ser	Gly	Glu	Lys	Asn	
104					160					165				170			
106	ggg	tta	ata	ctg	gag	aag	cct	tat	tat	atg	ggc	gag	tca	ctt	aat	gga	640
107	Gly	Leu	Ile	Leu	Glu	Lys	Pro	Tyr	Tyr	Met	Gly	Glu	Ser	Leu	Asn	Gly	
108			175					180				185					
110	aga	tta	ggt	ctg	gac	att	aat	gta	gag	aag	aaa	ctt	gtg	gag	gca	aaa	688
111	Arg	Leu	Gly	Leu	Asp	Ile	Asn	Val	Glu	Lys	Lys	Leu	Val	Glu	Ala	Lys	
112		190						195				200					
114	atc	aat	gaa	ctt	caa	gca	gcg	ggg	gca	acg	gaa	aag	tcc	att	aaa	tcg	736
115	Ile	Asn	Glu	Leu	Gln	Ala	Ala	Gly	Ala	Thr	Glu	Lys	Ser	Ile	Lys	Ser	
116		205						210				215					
118	aca	atg	aag	gac	atg	ggc	atc	gag	agg	gca	aga	cac	tgg	gga	tgg	cca	784
119	Thr	Met	Lys	Asp	Met	Gly	Ile	Glu	Arg	Ala	Arg	His	Trp	Gly	Trp	Pro	
120	220					225						230				235	
122	aat	gtg	tat	gta	ttc	acc	aag	gca	tta	ggg	gag	atg	ctt	ttg	atg	caa	832
123	Asn	Val	Tyr	Val	Phe	Thr	Lys	Ala	Leu	Gly	Glu	Met	Leu	Leu	Met	Gln	
124				240						245			250				
126	tac	aaa	ggg	gac	att	ccg	ctt	act	att	att	cgt	ccc	acc	atc	atc	acc	880
127	Tyr	Lys	Gly	Asp	Ile	Pro	Leu	Thr	Ile	Ile	Arg	Pro	Thr	Ile	Ile	Thr	
128				255					260					265			

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TIME: 13:10:45

Input Set : A:\1651802.app

Output Set: N:\CRF4\08182003\H657749C.raw

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131 Ser Thr Phe Lys Glu Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr
132      270      275      280
134 atc gat aat gta cct gta tat tat ggt aaa ggg aga ttg agg tgt atg 976
135 Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met
136      285      290      295
138 ctt tgc gga ccc agc aca ata att gac ctg ata ccg gca gat atg gtc 1024
139 Leu Cys Gly Pro Ser Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val
140 300      305      310      315
142 gtg aat gca acg ata gta gcc atg gtg gcg cac gca aac caa aga tac 1072
143 Val Asn Ala Thr Ile Val Ala Met Val Ala His Ala Asn Gln Arg Tyr
144      320      325      330
146 gta gag ccg gtg aca tac cat gtg gga tct tca gcg gcg aat cca atg 1120
147 Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met
148      335      340      345
150 aaa ctg agt gca tta cca gag atg gca cac cgt tac ttc acc aag aat 1168
151 Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn
152      350      355      360
154 cca tgg atc aac ccg gat cgc aac cca gta cat gtg ggt cgg gct atg 1216
155 Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met
156      365      370      375
158 gtc ttc tcc tcc ttc tcc acc ttc cac ctt tat ctc acc ctt aat ttc 1264
159 Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe
160 380      385      390      395
162 ctc ctt cct ttg aag gta ctg gag ata gca aat aca ata ttc tgc caa 1312
163 Leu Leu Pro Leu Lys Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln
164      400      405      410
166 tgg ttc aag ggt aag tac atg gat ctt aaa agg aag acg agg ttg ttg 1360
167 Trp Phe Lys Gly Lys Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu
168      415      420      425
170 ttg cgt tta gta gac att tat aaa ccc tac ctc ttc ttc caa ggc atc 1408
171 Leu Arg Leu Val Asp Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile
172      430      435      440
174 ttt gat gac atg aac act gag aag ttg cgg att gct gca aaa gaa agc 1456
175 Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser
176      445      450      455
178 ata gtt gaa gct gat atg ttt tac ttt gat ccc agg gca att aac tgg 1504
179 Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp
180 460      465      470      475
W--> 182 gaa gat tac ttc ttg aaa act cat ttc cca ggn gtc gta gag cac gtt 1552
183 Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
184      480      485      490
186 ctt aac taaaagttac ggtacgaaaa tgagaagatt ggaatgcatg caccgaaagn 1608
187 Leu Asn
189 ncaacataaaa agacgtggtt aaagtcatgg tcaaaaaaaga aataaaatgc agtttaggttt 1668
191 gtgttgacgt tttgattcct tgtattgtta cttgtacttt tgatcttttt cttttttaat 1728
193 gaaatttctc tctttgtttt gtgaaaaaaa aaaaaaaaaa gagctcctgc agaagctt 1786
196 <210> SEQ ID NO: 2
197 <211> LENGTH: 493

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## RAW SEQUENCE LISTING

DATE: 08/18/2003

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TIME: 13:10:45

Input Set : A:\1651802.app

Output Set: N:\CRF4\08182003\H657749C.raw

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198 <212> TYPE: PRT
199 <213> ORGANISM: Simmondsia chinensis
201 <400> SEQUENCE: 2
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205 Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys Ile Phe Val Glu Lys
206 20 25 30
208 Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu Tyr Leu Leu Leu Arg
209 35 40 45
211 Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu Gln Asn Glu Val Phe
212 50 55 60
214 Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn Leu Gly Ala Asn Phe
215 65 70 75 80
217 Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val Pro Gly Asp Ile Thr
218 85 90 95
220 Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu Lys Glu Glu Met Trp
221 100 105 110
223 Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala Thr Ile Asn Phe Ile
224 115 120 125
226 Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr Tyr Gly Ala Lys Tyr
227 130 135 140
229 Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu Lys Ile Phe Val His
230 145 150 155 160
232 Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn Gly Leu Ile Leu Glu
233 165 170 175
235 Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly Arg Leu Gly Leu Asp
236 180 185 190
238 Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys Ile Asn Glu Leu Gln
239 195 200 205
241 Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser Thr Met Lys Asp Met
242 210 215 220
244 Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro Asn Val Tyr Val Phe
245 225 230 235 240
247 Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln Tyr Lys Gly Asp Ile
248 245 250 255
250 Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr Ser Thr Phe Lys Glu
251 260 265 270
253 Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr Ile Asp Asn Val Pro
254 275 280 285
256 Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met Leu Cys Gly Pro Ser
257 290 295 300
259 Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val Val Asn Ala Thr Ile
260 305 310 315 320
262 Val Ala Met Val Ala His Ala Asn Gln Arg Tyr Val Glu Pro Val Thr
263 325 330 335
265 Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met Lys Leu Ser Ala Leu
266 340 345 350
268 Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn Pro Trp Ile Asn Pro
269 355 360 365

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## RAW SEQUENCE LISTING

DATE: 08/18/2003

PATENT APPLICATION: US/08/657,749C

TIME: 13:10:45

Input Set : A:\1651802.app

Output Set: N:\CRF4\08182003\H657749C.raw

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271 Asp Arg Asn Pro Val His Val Gly Arg Ala Met Val Phe Ser Ser Phe
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274 Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe Leu Leu Pro Leu Lys
275 385      390      395      400
277 Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln Trp Phe Lys Gly Lys
278      405      410      415
280 Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu Leu Arg Leu Val Asp
281      420      425      430
283 Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile Phe Asp Asp Met Asn
284      435      440      445
286 Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser Ile Val Glu Ala Asp
287      450      455      460
289 Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp Glu Asp Tyr Phe Leu
290 465      470      475      480
292 Lys Thr His Phe Pro Gly Val Val Glu His Val Leu Asn
293      485      490
297 <210> SEQ ID NO: 3
298 <211> LENGTH: 1733
299 <212> TYPE: DNA
300 <213> ORGANISM: Simmondsia chinensis
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303 <221> NAME/KEY: CDS
304 <222> LOCATION: (39)..(1610)
306 <220> FEATURE:
307 <221> NAME/KEY: modified_base
308 <222> LOCATION: (676)
309 <223> OTHER INFORMATION: a, c, t, or g
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313                               Met Lys Ala Lys Thr Ile
314                               1 5
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317 Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr
318      10      15      20
320 act atg acc gcc act ctc ccc aac ttc aag tcc tcc atc aac tta cac 152
321 Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His
322      25      30      35
324 cac gtc aag ctc ggc tac cac tac tta atc tcc aat gcc ctc ttc ctc 200
325 His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu
326      40      45      50
328 gta ttc atc ccc ctt ttg ggc ctc gct tcg gcc cat ctc tcc tcc ttc 248
329 Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His Leu Ser Ser Phe
330 55      60      65      70
332 tcg gcc cat gac ttg tcc ctg ctc ttc gac ctc ctt cgc cgc aac ctc 296
333 Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu
334      75      80      85
336 ctc cct gtt gtc gtt tgt tct ttc ctc ttc gtt tta tta gca acc cta 344
337 Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu
338      90      95      100

```

*what about "n" at location 737?*

*(see p6)*

08/657,749C 6

agc ttg ttt aac cca acg ccg tgg ctg tca tcc atg ata gtt aac cat 728  
 Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His  
 215 220 225 230  
 tac aag ctn agg ggt aat ata ctt agc tat aat ctt ggt ggc atg ggt 776  
 Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly  
 235 240 245

"n"  
 location

see p. 7 for more errors

08/657,749c 7

<210> SEQ ID NO 4  
<211> LENGTH: 524  
<212> TYPE: PRT  
<213> ORGANISM: Simmondsia chinensis  
<220> FEATURE:  
<221> NAME/KEY: MOD\_RES  
<222> LOCATION: (213)  
<223> OTHER INFORMATION: Variable amino acid  
<400> SEQUENCE: 4

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Met Thr Thr Thr Thr Thr Met Thr Ala Thr Leu Pro Asn Phe Lys  
20 25 30  
Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile  
35 40 45  
Ser Asn Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser  
50 55 60  
Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp  
65 70 75 80  
Leu Leu Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe  
85 90 95  
Val Leu Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr  
100 105 110  
Leu Val Asp Phe Gly Cys Tyr Lys Pro Gln Pro Asn Leu Met Thr Ser  
115 120 125  
His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys  
130 135 140  
Glu Asn Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly  
145 150 155 160  
Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Ala Glu Pro  
165 170 175  
Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala  
180 185 190  
Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly  
195 200 205  
Ile Leu Val Val Xaa Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser  
210 215 220  
Ser Met Ile Val Asn His Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr  
225 230 235 240

what about Xaa at location 233?

see  
below

↑

see p. 8



8

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/08/657,749C

DATE: 08/18/2003  
TIME: 13:10:46

Input Set : A:\1651802.app  
Output Set: N:\CRF4\08182003\H657749C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1537,1608,1609  
Seq#:3; N Pos. 676,737  
Seq#:3; Xaa Pos. 213,233  
Seq#:4; Xaa Pos. 213,233  
Seq#:22; N Pos. 345  
Seq#:22; Xaa Pos. 102  
Seq#:23; Xaa Pos. 102  
Seq#:24; N Pos. 155,217  
Seq#:24; Xaa Pos. 51,72  
Seq#:25; Xaa Pos. 51,72  
Seq#:31; Xaa Pos. 3,10  
Seq#:35; Xaa Pos. 4,5  
Seq#:36; Xaa Pos. 7,8,11  
Seq#:38; Xaa Pos. 1,17  
Seq#:39; Xaa Pos. 7  
Seq#:42; N Pos. 9,12,15  
Seq#:43; N Pos. 15  
Seq#:46; Xaa Pos. 3  
Seq#:47; N Pos. 30,33  
Seq#:49; N Pos. 30,33,36  
Seq#:50; N Pos. 29,32,35  
Seq#:52; N Pos. 39  
Seq#:53; N Pos. 27

*Please ensure these n/Xaa  
locations are explained*